

## SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: VAN ALYSTYNE, Diane  
SHARMA, Lawrence Rajendra
- (ii) TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR CARRIER, ANTIBODIES THERETO, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 75
- (iv) CORRESPONDENCE ADDRESS:  
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Street, N.W., Suite 500  
(C) CITY: San Diego Washington  
(D) STATE: California D.C.  
(E) COUNTRY: USA  
(F) ZIP: 92037 20007-5109
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 09/489,850 08/486,050  
(B) FILING DATE: 24-JAN-2000 07 JUN 1995  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/486,050  
(B) FILING DATE: 07-JUN-1995  
(C) APPLICATION NUMBER: US 08/127,499  
(D) FILING DATE: 28-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:  
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Bern, Stephen A.  
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(C) REFERENCE/DOCKET NUMBER: ANALYSTYNE-P001  
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 992 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Ser Thr Thr Pro Ile Thr Met Glu Asp Leu Gln Lys Ala Leu  
1 5 10 15  
Glu Ala Gln Ser Arg Ala Leu Arg Ala Gly Leu Ala Ala Gly Ala Ser  
20 25 30

Gln Ser Arg Arg Pro Arg Pro Pro Arg His Ala Arg Leu Gln His Leu  
 35 40 45  
 Pro Glu Met Thr Pro Ala Val Thr Pro Glu Gly Pro Ala Pro Pro Arg  
 50 55 60  
 Thr Gly Ala Trp Gln Arg Lys Asp Trp Ser Arg Ala Pro Pro Pro Pro  
 65 70 75 80  
 Glu Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro Ser  
 85 90 95  
 Arg Ala Pro Pro Gln Gln Pro Gln Pro Pro Arg Met Gln Thr Gly Arg  
 100 105 110  
 Gly Gly Ser Ala Pro Arg Pro Glu Leu Gly Pro Pro Thr Asn Pro Phe  
 115 120 125  
 Gln Ala Ala Val Ala Arg Gly Leu Arg Pro Pro Leu His Asp Pro Asp  
 130 135 140  
 Thr Glu Ala Pro Thr Glu Ala Cys Val Thr Ser Trp Leu Trp Ser Glu  
 145 150 155 160  
 Gly Glu Gly Ala Val Phe Tyr Arg Val Asp Leu His Phe Ile Asn Leu  
 165 170 175  
 Gly Thr Pro Pro Leu Asp Glu Asp Gly Arg Trp Asp Pro Ala Leu Met  
 180 185 190  
 Tyr Asn Pro Cys Gly Pro Glu Pro Pro Ala His Val Val Arg Ala Tyr  
 195 200 205  
 Asn Gln Pro Ala Gly Asp Val Arg Gly Val Trp Gly Lys Gly Glu Arg  
 210 215 220  
 Thr Tyr Ala Glu Gln Asp Phe Arg Val Gly Gly Thr Arg Trp His Arg  
 225 230 235 240  
 Leu Leu Arg Met Pro Val Arg Gly Leu Asp Gly Asp Thr Ala Pro Leu  
 245 250 255  
 Pro Pro His Thr Thr Glu Arg Ile Glu Thr Arg Ser Ala Arg His Pro  
 260 265 270  
 Trp Arg Ile Arg Phe Gly Ala Pro Gln Ala Phe Leu Ala Gly Leu Leu  
 275 280 285  
 Leu Ala Ala Val Ala Val Gly Thr Ala Arg Ala Gly Leu Gln Pro Arg  
 290 295 300  
 Ala Asp Met Ala Ala Pro Pro Met Pro Pro Gln Pro Pro Arg Ala His  
 305 310 315 320  
 Gly Gln His Tyr Gly His His His His Gln Leu Pro Phe Leu Gly His  
 325 330 335  
 Asp Gly His His Gly Gly Thr Leu Arg Val Gly Gln His His Arg Asn  
 340 345 350  
 Ala Ser Asp Val Leu Pro Gly His Trp Leu Gln Gly Gly Trp Gly Cys  
 355 360 365  
 Tyr Asn Leu Ser Asp Trp His Gln Gly Thr His Val Cys His Thr Lys  
 370 375 380

His Met Asp Phe Trp Cys Val Glu His Asp Arg Pro Pro Pro Ala Thr  
 385 390 395 400  
 Pro Thr Ser Leu Thr Thr Ala Ala Asn Tyr Ile Ala Ala Ala Thr Pro  
 405 410 415  
 Ala Thr Ala Pro Pro Cys His Ala Gly Leu Asn Asp Ser Cys Gly  
 420 425 430  
 Gly Phe Leu Ser Gly Cys Gly Pro Met Arg Leu Pro Thr Ala Leu Thr  
 435 440 445  
 Pro Gly Ala Val Gly Asp Leu Arg Ala Val His His Arg Pro Val Pro  
 450 455 460  
 Ala Tyr Pro Val Cys Cys Ala Met Arg Trp Gly Leu Pro Pro Trp Glu  
 465 470 475 480  
 Leu Val Ile Leu Thr Ala Arg Pro Glu Asp Gly Trp Thr Cys Arg Gly  
 485 490 495  
 Val Pro Ala His Pro Gly Thr Arg Cys Pro Glu Leu Val Ser Pro Met  
 500 505 510  
 Gly Arg Ala Thr Cys Ser Pro Ala Ser, Ala Leu Trp Leu Ala Thr Ala  
 515 520 525  
 Asn Ala Leu Ser Leu Asp His Ala Phe Ala Ala Phe Val Leu Leu Val  
 530 535 540  
 Pro Trp Val Leu Ile Phe Met Val Cys Arg Arg Ala Cys Arg Arg Pro  
 545 550 555 560  
 Ala Pro Pro Pro Pro Ser Pro Gln Ser Ser Cys Arg Gly Thr Thr Pro  
 565 570 575  
 Pro Ala Tyr Gly Glu Glu Ala Phe Thr Tyr Leu Cys Thr Ala Pro Gly  
 580 585 590  
 Cys Ala Thr Gln Thr Pro Val Pro Val Arg Leu Ala Gly Val Gly Phe  
 595 600 605  
 Glu Ser Lys Ile Val Asp Gly Gly Cys Phe Ala Pro Trp Asp Leu Glu  
 610 615 620  
 Ala Thr Gly Ala Cys Ile Cys Glu Ile Pro Thr Asp Val Ser Cys Glu  
 625 630 635 640  
 Gly Leu Gly Ala Trp Val Pro Thr Ala Pro Cys Ala Arg Ile Trp Asn  
 645 650 655  
 Gly Thr Gln Arg Ala Cys Thr Phe Trp Ala Val Asn Ala Tyr Ser Ser  
 660 665 670  
 Gly Gly Tyr Ala Gln Leu Ala Ser Tyr Phe Asn Pro Gly Gly Ser Tyr  
 675 680 685  
 Tyr Lys Gln Tyr His Pro Thr Ala Cys Glu Val Glu Pro Ala Phe Gly  
 690 695 700  
 His Ser Asp Ala Ala Cys Trp Gly Phe Pro Thr Asp Thr Val Met Ser  
 705 710 715 720  
 Val Phe Ala Leu Ala Ser Tyr Val Gln His Pro His Lys Thr Val Arg  
 725 730 735

Val Lys Phe His Thr Glu Thr Arg Thr Val Trp Gln Leu Ser Val Ala  
740 745 750

Gly Val Ser Cys Asn Val Thr Thr Glu His Pro Phe Cys Asn Thr Pro  
755 760 765

His Gly Gln Leu Glu Val Gln Val Pro Pro Asp Pro Gly Asp Leu Val  
770 775 780

Glu Tyr Ile Met Asn Tyr Thr Gly Asn Gln Gln Ser Arg Trp Gly Leu  
785 790 795 800

Gly Ser Pro Asn Cys His Gly Pro Asp Trp Ala Ser Pro Val Cys Gln  
805 810 815

Arg His Ser Pro Asp Cys Ser Arg Leu Val Gly Ala Thr Pro Glu Arg  
820 825 830

Pro Arg Leu Arg Leu Val Asp Ala Asp Asp Pro Leu Leu Arg Thr Ala  
835 840 845

Pro Gly Pro Gly Glu Val Trp Val Thr Pro Val Ile Gly Ser Gln Ala  
850 855 860

Arg Lys Cys Gly Leu His Ile Arg Ala, Gly Pro Tyr Gly His Ala Thr  
865 870 875 880

Val Glu Met Pro Glu Trp Ile His Ala His Thr Thr Ser Asp Pro Trp  
885 890 895

His Pro Pro Gly Pro Leu Gly Leu Lys Phe Lys Thr Val Arg Pro Val  
900 905 910

Ala Leu Pro Arg Ala Leu Ala Pro Pro Arg Asn Val Arg Val Thr Gly  
915 920 925

Cys Tyr Gln Cys Gly Thr Pro Ala Leu Val Glu Gly Leu Ala Pro Gly  
930 935 940

Gly Gly Asn Cys His Leu Thr Val Asn Gly Glu Asp Val Gly Ala Phe  
945 950 955 960

Pro Pro Gly Lys Phe Val Thr Ala Ala Leu Leu Asn Thr Pro Pro Pro  
965 970 975

Tyr Gln Val Ser Cys Gly Gly Glu Ser Asp Arg Ala Ser Ala Gly His  
980 985 990

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Ser Arg Ala Pro Pro Gln Gln Pro Gln Pro Pro Arg Met Gln Thr  
1 5 10 15

Gly Arg Gly Gly Ser  
20

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Pro Gln Pro Pro Arg Met  
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Clu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro Ser Arg  
1 5 10 15

Ala Pro Pro Gln Gln  
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Thr Pro Ala Pro Lys Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Met Ala Ala Pro Pro Met Pro Pro Gln Pro Pro Arg Ala His Gly  
1 5 10 15  
Gln His Tyr Gly His  
20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Pro Gln Pro Pro Arg Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1063 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ser Thr Thr Pro Ile Thr Met Glu Asp Leu Gln Lys Ala Leu  
1 5 10 15  
Glu Ala Gln Ser Arg Ala Leu Arg Ala Glu Leu Ala Ala Gly Ala Ser  
20 25 30  
Gln Ser Arg Arg Pro Arg Pro Pro Arg Gln Arg Asp Ser Ser Thr Ser  
35 40 45  
Gly Asp Asp Ser Gly Arg Asp Ser Gly Gly Pro Arg Arg Arg Gly  
50 55 60  
Asn Arg Gly Arg Gly Gln Arg Arg Asp Trp Ser Arg Ala Pro Pro Pro  
65 70 75 80  
Pro Glu Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro  
85 90 95  
Ser Arg Ala Pro Pro Gln Gln Pro Gln Pro Pro Arg Met Gln Thr Gly  
100 105 110  
Arg Gly Gly Ser Ala Pro Arg Pro Glu Leu Gly Pro Pro Thr Asn Pro  
115 120 125  
Phe Gln Ala Ala Val Ala Arg Gly Leu Arg Pro Pro Leu His Asp Pro  
130 135 140

Asp Thr Glu Ala Pro Thr Glu Ala Cys Val Thr Ser Trp Leu Trp Ser  
 145 150 155 160  
 Glu Gly Gln Gly Ala Val Phe Tyr Arg Val Asp Leu His Phe Thr Asn  
 165 170 175  
 Leu Gly Thr Pro Pro Leu Asp Glu Asp Gly Arg Trp Asp Pro Ala Leu  
 180 185 190  
 Met Tyr Asn Pro Cys Gly Pro Glu Pro Pro Ala His Val Val Arg Ala  
 195 200 205  
 Tyr Asn Gln Pro Ala Gly Asp Val Arg Gly Val Trp Gly Lys Gly Glu  
 210 215 220  
 Arg Thr Tyr Ala Glu Gln Asp Phe Arg Val Gly Gly Thr Arg Trp His  
 225 230 235 240  
 Arg Leu Leu Arg Met Pro Val Arg Gly Leu Asp Gly Asp Ser Ala Pro  
 245 250 255  
 Leu Pro Pro His Thr Thr Glu Arg Ile Glu Thr Arg Ser Ala Arg His  
 260 265 270  
 Pro Trp Arg Ile Arg Phe Gly Ala Pro Gln Ala Phe Leu Ala Gly Leu  
 275 280 285  
 Leu Leu Ala Thr Val Ala Val Gly Thr Ala Arg Ala Gly Leu Gln Pro  
 290 295 300  
 Arg Ala Asp Met Ala Ala Pro Pro Thr Leu Pro Gln Pro Pro Cys Ala  
 305 310 315 320  
 His Gly Gln His Tyr Gly His His His His Gln Leu Pro Phe Leu Gly  
 325 330 335  
 His Asp Gly His His Gly Gly Thr Leu Arg Val Gly Gln His Tyr Arg  
 340 345 350  
 Asn Ala Ser Asp Val Leu Pro Gly His Trp Leu Gln Gly Gly Trp Gly  
 355 360 365  
 Cys Tyr Asn Leu Ser Asp Trp His Gln Gly Thr His Val Cys His Thr  
 370 375 380  
 Lys His Met Asp Phe Trp Cys Val Glu His Ala Arg Pro Pro Pro Ala  
 385 390 395 400  
 Thr Pro Thr Pro Leu Thr Thr Ala Ala Asn Ser Thr Thr Ala Ala Thr  
 405 410 415  
 Pro Ala Thr Ala Pro Ala Pro Cys His Ala Gly Leu Asn Asp Ser Cys  
 420 425 430  
 Gly Gly Phe Leu Ser Gly Cys Gly Pro Met Arg Leu Arg His Gly Ala  
 435 440 445  
 Asp Thr Arg Cys Gly Arg Leu Ile Cys Gly Leu Ser Thr Thr Ala Gln  
 450 455 460  
 Tyr Pro Pro Thr Arg Phe Gly Cys Ala Met Arg Trp Gly Leu Pro Pro  
 465 470 475 480  
 Trp Glu Leu Val Val Leu Thr Ala Arg Pro Glu Asp Gly Trp Thr Cys  
 485 490 495

Arg Gly Val Pro Ala His Pro Gly Ala Arg Cys Pro Glu Leu Val Ser  
 500 505 510  
 Pro Met Gly Arg Ala Thr Cys Ser Pro Ala Ser Ala Leu Trp Leu Ala  
 515 520 525  
 Thr Ala Asn Ala Leu Ser Leu Asp His Ala Leu Ala Phe Val Leu  
 530 535 540  
 Ser Val Pro Trp Val Leu Ile Phe Met Val Cys Arg Arg Ala Cys Arg  
 545 550 555 560  
 Arg Arg Gly Ala Ala Ala Ala Leu Thr Ala Val Val Leu Gln Gly Tyr  
 565 570 575  
 Asn Pro Pro Ala Tyr Gly Glu Glu Ala Phe Thr Tyr Leu Cys Thr Ala  
 580 585 590  
 Pro Gly Cys Ala Thr Gln Ala Pro Val Pro Val Arg Leu Ala Gly Val  
 595 600 605  
 Arg Phe Glu Ser Lys Ile Val Asp Gly Gly Cys Phe Ala Pro Trp Asp  
 610 615 620  
 Leu Glu Ala Thr Gly Ala Cys Ile Cys Glu Ile Pro Thr Asp Val Ser  
 625 630 635 640  
 Cys Glu Gly Leu Gly Ala Trp Val Pro Ala Ala Pro Cys Ala Arg Ile  
 645 650 655  
 Trp Asn Gly Thr Gln Arg Ala Cys Thr Phe Trp Ala Val Asn Ala Tyr  
 660 665 670  
 Ser Ser Gly Gly Tyr Ala Gln Leu Ala Ser Tyr Phe Asn Pro Gly Gly  
 675 680 685  
 Ser Tyr Tyr Lys Gln Tyr His Pro Thr Ala Cys Glu Val Glu Pro Ala  
 690 695 700  
 Phe Gly His Ser Asp Ala Ala Cys Trp Gly Phe Pro Thr Asp Thr Val  
 705 710 715 720  
 Met Ser Val Phe Ala Leu Ala Ser Tyr Val Gln His Pro His Lys Thr  
 725 730 735  
 Val Arg Val Lys Phe His Thr Glu Thr Arg Thr Val Trp Gln Leu Ser  
 740 745 750  
 Val Ala Gly Val Ser Cys Asn Val Thr Thr Glu His Pro Phe Cys Asn  
 755 760 765  
 Thr Pro His Gly Gln Leu Glu Val Gln Val Pro Pro Asp Pro Gly Asp  
 770 775 780  
 Leu Val Glu Tyr Ile Met Asn Tyr Thr Gly Asn Gln Gln Ser Arg Trp  
 785 790 795 800  
 Gly Leu Gly Ser Pro Asn Cys His Gly Pro Asp Trp Ala Ser Pro Val  
 805 810 815  
 Cys Gln Arg His Ser Pro Asp Cys Ser Arg Leu Val Gly Ala Thr Pro  
 820 825 830  
 Glu Arg Pro Arg Leu Arg Leu Val Asp Ala Asp Asp Pro Leu Leu Arg  
 835 840 845



Thr Ala Pro Gly Pro Gly Glu Val Trp Val Thr Pro Val Ile Gly Ser  
 850 855 860  
 Gln Ala Arg Lys Cys Gly Leu His Ile Arg Ala Gly Pro Tyr Gly His  
 865 870 875 880  
 Ala Thr Val Glu Met Pro Glu Trp Ile His Ala His Thr Thr Ser Asp  
 885 890 895  
 Pro Trp His Pro Pro Gly Pro Leu Gly Leu Lys Phe Lys Thr Val Arg  
 900 905 910  
 Pro Val Ala Leu Pro Arg Thr Leu Ala Pro Pro Arg Asn Val Arg Val  
 915 920 925  
 Thr Gly Cys Tyr Gln Cys Gly Thr Pro Ala Leu Val Glu Gly Leu Ala  
 930 935 940  
 Pro Gly Gly Gly Asn Cys His Leu Thr Val Asn Gly Glu Asp Val Gly  
 945 950 955 960  
 Ala Val Pro Pro Gly Lys Phe Val Thr Ala Ala Leu Leu Asn Thr Pro  
 965 970 975  
 Pro Pro Tyr Gln Val Ser Cys Gly Gly Glu Ser Asp Arg Ala Ser Ala  
 980 985 990  
 Arg Val Ile Asp Pro Ala Ala Gln Ser Phe Thr Gly Val Val Tyr Gly  
 995 1000 1005  
 Thr His Thr Thr Ala Val Ser Glu Thr Arg Gln Thr Trp Ala Glu Trp  
 1010 1015 1020  
 Ala Ala Ala His Trp Trp Gln Leu Thr Leu Gly Ala Thr Cys Ala Leu  
 1025 1030 1035 1040  
 Pro Leu Ala Gly Leu Leu Ala Cys Cys Ala Lys Cys Leu Tyr Tyr Leu  
 1045 1050 1055  
 Arg Gly Ala Ile Ala Pro Arg  
 1060

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Met Ala Ala Pro Pro Thr Leu Pro Gln Pro Pro Arg Ala His Gly  
 1 5 10 15  
 Gln His Tyr Gly His  
 20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Pro Gln Pro Pro Cys Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 478 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp  
1 5 10 15  
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys  
20 25 30  
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro  
35 40 45  
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu  
50 55 60  
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn  
65 70 75 80  
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp  
85 90 95  
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys  
100 105 110  
Lys Lys Ala Gln Gln Ala Ala Asp Thr Gly His Ser Ser Gln Val  
115 120 125  
Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His  
130 135 140  
Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu  
145 150 155 160  
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser  
165 170 175  
Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly  
180 185 190  
Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu  
195 200 205  
Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala  
210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr  
 225 230 235 240  
 Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile  
 245 250 255  
 Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys  
 260 265 270  
 Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly  
 275 280 285  
 Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu  
 290 295 300  
 Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr  
 305 310 315 320  
 Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala  
 325 330 335  
 Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly  
 340 345 350  
 Val Gly Gly Pro Gly His Lys Ala Arg, Val Leu Ala Glu Ala Met Ser  
 355 360 365  
 Gln Val Thr Asn Thr Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg  
 370 375 380  
 Asn Gln Arg Lys Met Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His  
 385 390 395 400  
 Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys  
 405 410 415  
 Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn  
 420 425 430  
 Phe Leu Gly Lys Ile Cys Leu Pro Thr Arg Glu Gly Gln Gly Ile Phe  
 435 440 445  
 Phe Arg Ala Asp Gln Ser Gln Gln Pro His His Phe Arg Ala Asp  
 450 455 460  
 Gln Ser Gln Gln Pro His Gln Lys Arg Ala Ser Gly Leu Gly  
 465 470 475

(2) INFORMATION FOR SEQ ID NO:12:

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn  
 1 5 10 15  
 Ala Trp Val Lys Val  
 20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gln Ala Ile Ser Pro Arg Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 861 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys  
1 5 10 15  
Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu  
20 25 30  
Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala  
35 40 45  
Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu  
50 55 60  
Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn  
65 70 75 80  
Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp  
85 90 95  
Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp  
100 105 110  
Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser  
115 120 125  
Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn  
130 135 140  
Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys  
145 150 155 160  
Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys  
165 170 175  
Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp  
180 185 190

Thr Thr Ser Tyr Thr Leu Thr Ser Cys Asn Thr Ser Val Ile Thr Gln  
 195 200 205  
 Ala Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala  
 210 215 220  
 Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly  
 225 230 235 240  
 Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile  
 245 250 255  
 Arg Pro Val Val Ser Thr Gln Leu Leu Leu Asn Gly Ser Leu Ala Glu  
 260 265 270  
 Glu Glu Val Val Ile Arg Ser Ala Asn Phe Thr Asp Asn Ala Lys Thr  
 275 280 285  
 Ile Ile Val Gln Leu Asn Gln Ser Val Glu Ile Asn Cys Thr Arg Pro  
 290 295 300  
 Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg  
 305 310 315 320  
 Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys  
 325 330 335  
 Asn Ile Ser Arg Ala Lys Trp Asn Ala Thr Leu Lys Gln Ile Ala Ser  
 340 345 350  
 Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln  
 355 360 365  
 Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly  
 370 375 380  
 Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp  
 385 390 395 400  
 Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser  
 405 410 415  
 Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Phe Ile Asn Met Trp  
 420 425 430  
 Gln Glu Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile  
 435 440 445  
 Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly  
 450 455 460  
 Asn Asn Asn Asn Gly Ser Glu Ile Phe Arg Pro Gly Gly Gly Asp Met  
 465 470 475 480  
 Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile  
 485 490 495  
 Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln  
 500 505 510  
 Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu  
 515 520 525  
 Gly Ala Ala Gly Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val  
 530 535 540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu  
 545 550 555 560  
 Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp  
 565 570 575  
 Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu  
 580 585 590  
 Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile  
 595 600 605  
 Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu  
 610 615 620  
 Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile  
 625 630 635 640  
 Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn  
 645 650 655  
 Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala  
 660 665 670  
 Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys  
 675 680 685  
 Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe  
 690 695 700  
 Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu  
 705 710 715 720  
 Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu  
 725 730 735  
 Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg  
 740 745 750  
 Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu  
 755 760 765  
 Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr  
 770 775 780  
 Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr  
 785 790 795 800  
 Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala  
 805 810 815  
 Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp  
 820 825 830  
 Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile  
 835 840 845  
 Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu  
 850 855 860

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Ser Leu Ile Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln  
1 5 10 15

Glu Leu Leu Glu Leu  
20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Asn Gln Gln Glu Lys Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 274 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Lys Thr Thr Leu Lys Met Thr Ala Leu Ala Ala Leu Ser Ala Phe  
1 5 10 15

Val Leu Ala Gly Cys Gly Ser His Gln Met Lys Ser Glu Glu His Ala  
20 25 30

Asn Met Gln Leu Gln Gln Gln Ala Val Leu Gly Leu Asn Trp Met Gln  
35 40 45

Asp Ser Gly Glu Tyr Lys Ala Leu Ala Tyr Gln Ala Tyr Asn Ala Ala  
50 55 60

Lys Val Ala Phe Asp His Ala Lys Val Ala Lys Gly Lys Lys Lys Ala  
65 70 75 80

Val Val Ala Asp Leu Asp Glu Thr Met Leu Asp Asn Ser Pro Tyr Ala  
85 90 95

Gly Trp Gln Val Gln Asn Asn Lys Pro Phe Asp Gly Lys Asp Trp Thr  
100 105 110

Arg Trp Val Asp Ala Arg Gln Ser Arg Ala Val Pro Gly Ala Val Glu  
115 120 125

Phe Asn Asn Tyr Val Asn Ser His Asn Gly Lys Val Phe Tyr Val Thr  
 130 135 140  
 Asn Arg Lys Asp Ser Thr Glu Lys Ser Gly Thr Ile Asp Asp Met Lys  
 145 150 155 160  
 Arg Leu Gly Phe Asn Gly Val Glu Glu Ser Ala Phe Tyr Leu Lys Lys  
 165 170 175  
 Asp Lys Ser Ala Lys Ala Ala Arg Phe Ala Glu Ile Glu Lys Gln Gly  
 180 185 190  
 Tyr Glu Ile Val Leu Tyr Val Gly Asp Asn Leu Asp Asp Phe Gly Asn  
 195 200 205  
 Thr Val Tyr Gly Lys Leu Asn Ala Asp Arg Arg Ala Phe Val Asp Gln  
 210 215 220  
 Asn Gln Gly Lys Phe Gly Lys Thr Phe Ile Met Leu Pro Asn Ala Asn  
 225 230 235 240  
 Tyr Gly Gly Trp Glu Gly Gly Leu Ala Glu Gly Tyr Phe Lys Lys Asp  
 245 250 255  
 Thr Gln Gly Gln Ile Lys Ala Arg Leu Asp Ala Val Gln Ala Trp Asp  
 260 265 270  
 Gly Lys

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Ser Pro Tyr Ala Gly Trp Gln Val Gln Asn Asn Lys Pro Phe Asp  
 1 5 10 15  
 Gly Lys Asp Trp Thr  
 20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gln Val Gln Asn Asn Lys Pro  
 1 5



(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Ile Gln Pro Pro Lys Asn Leu Leu Phe Ser Ser Leu Leu Phe Ser Ser
 1              5              10              15
Leu Leu Phe Ser Ser Ala Ala Gln Ala Ala Ser Glu Asp Arg Arg Ser
              20              25              30
Pro Tyr Tyr Val Gln Ala Asp Leu Ala Tyr Ala Ala Glu Arg Ile Thr
 35              40              45
His Asp Tyr Pro Gln Ala Thr Gly Ala Asn Asn Thr Ser Thr Val Ser
 50              55              60
Asp Tyr Phe Arg Asn Ile Arg Ala His Ser Ile His Pro Arg Val Ser
 65              70              75              80
Val Gly Tyr Asp Phe Gly Gly Trp Arg Ile Ala Ala Asp Tyr Ala Ser
 85              90              95
Tyr Arg Lys Trp Asn Asn Asn Lys Tyr Ser Val Asn Thr Lys Glu Leu
100              105              110
Glu Asn Lys His Asn Asn Lys Lys Asp Leu Lys Thr Glu Asn Gln Glu
115              120              125
Asn Gly Thr Phe His Ala Ala Ser Ser Leu Gly Leu Ser Ala Ile Tyr
130              135              140
Asp Phe Lys Leu Lys Gly Lys Phe Lys Pro Tyr Ile Gly Ala Arg Val
145              150              155              160
Ala Tyr Gly His Val Arg His Ser Ile Asp
165              170
```

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Ile Gln Pro Pro Lys Asn Leu Leu Phe Ser Ser Leu Leu
 1              5              10
```

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Gln Pro Pro Lys Asn  
 1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 695 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Leu Met Ile Xaa Lys Phe Val Thr Lys Met Xaa Tyr Lys Thr Leu  
 1 5 10 15  
 Asp Lys Tyr Leu Arg Arg Arg Leu Ile Leu Asn Ile Ser Ile Val Xaa  
 20 25 30  
 Lys Xaa Leu Ser Glu Lys Arg Xaa Ile Xaa Met Asn Lys Lys Lys Met  
 35 40 45  
 Ile Leu Thr Ser Leu Ala Ser Val Ala Ile Leu Gly Ala Gly Phe Val  
 50 55 60  
 Ala Ser Gln Pro Thr Val Val Arg Ala Glu Glu Ser Pro Val Ala Ser  
 65 70 75 80  
 Gln Ser Lys Ala Glu Lys Asp Tyr Asp Ala Ala Lys Lys Asp Ala Lys  
 85 90 95  
 Asn Ala Lys Lys Ala Val Glu Asp Ala Gln Lys Ala Leu Asp Asp Ala  
 100 105 110  
 Lys Ala Ala Gln Lys Lys Tyr Asp Glu Asp Gln Lys Lys Thr Glu Glu  
 115 120 125  
 Lys Ala Ala Leu Glu Lys Ala Ala Ser Glu Glu Met Asp Lys Ala Val  
 130 135 140  
 Ala Ala Val Gln Gln Ala Tyr Leu Ala Tyr Gln Gln Ala Thr Asp Lys  
 145 150 155 160  
 Ala Ala Lys Asp Ala Ala Asp Lys Met Ile Asp Glu Ala Lys Lys Arg  
 165 170 175  
 Glu Glu Glu Ala Lys Thr Lys Phe Asn Thr Val Arg Ala Met Val Val  
 180 185 190  
 Pro Glu Pro Glu Gln Leu Ala Glu Thr Lys Lys Lys Ser Glu Glu Ala  
 195 200 205

Lys Gln Lys Ala Pro Glu Leu Thr Lys Lys Leu Glu Glu Ala Lys Ala  
 210 215 220  
 Lys Leu Glu Glu Ala Glu Lys Lys Ala Thr Glu Ala Lys Gln Lys Val  
 225 230 235 240  
 Asp Ala Glu Glu Val Ala Pro Gln Ala Lys Ile Ala Glu Leu Glu Asn  
 245 250 255  
 Gln Val His Arg Leu Glu Gln Glu Leu Lys Glu Ile Asp Glu Ser Glu  
 260 265 270  
 Ser Glu Asp Tyr Ala Lys Glu Gly Phe Arg Ala Pro Leu Gln Ser Lys  
 275 280 285  
 Leu Asp Ala Lys Lys Ala Lys Leu Ser Lys Leu Glu Glu Leu Ser Asp  
 290 295 300  
 Lys Ile Asp Glu Leu Asp Ala Glu Ile Ala Lys Leu Glu Asp Gln Leu  
 305 310 315 320  
 Lys Ala Ala Glu Glu Asn Asn Asn Val Glu Asp Tyr Phe Lys Glu Gly  
 325 330 335  
 Leu Glu Lys Thr Ile Ala Ala Lys Lys Ala Glu Leu Glu Lys Thr Glu  
 340 345 350  
 Ala Asp Leu Lys Lys Ala Val Asn Glu Pro Glu Lys Pro Ala Pro Ala  
 355 360 365  
 Pro Glu Thr Pro Ala Pro Glu Ala Pro Ala Glu Gln Pro Lys Pro Ala  
 370 375 380  
 Pro Ala Pro Gln Pro Ala Pro Ala Pro Lys Pro Glu Lys Pro Ala Glu  
 385 390 395 400  
 Gln Pro Lys Pro Glu Lys Thr Asp Asp Gln Gln Ala Glu Glu Asp Tyr  
 405 410 415  
 Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg Leu Thr Gln Gln Gln Pro  
 420 425 430  
 Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro Lys Thr Gly Trp Lys Gln  
 435 440 445  
 Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Thr  
 450 455 460  
 Gly Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ser Asn Gly  
 465 470 475 480  
 Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu  
 485 490 495  
 Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser  
 500 505 510  
 Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Leu Gln  
 515 520 525  
 Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr  
 530 535 540  
 Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly  
 545 550 555 560

Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu  
565 570 575

Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser  
580 585 590

Trp Tyr Tyr Trp Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Val Lys  
595 600 605

Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala  
610 615 620

Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu  
625 630 635 640

Gly Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala  
645 650 655

Asn Gly Glu Trp Val Xaa Ala Asp Xaa Ile Lys Ala Cys Xaa Glu His  
660 665 670

Leu Thr Phe Xaa Phe Xaa Asn Lys Asp Lys Val Arg Leu Asn Arg Phe  
675 680 685

Met Phe Val Phe Phe Arg Tyr  
690 695

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Glu Gln Tyr Asn Arg Leu Thr Gln Gln Gln Pro Pro Lys Ala Glu Lys  
1 5 10 15

Pro Ala Pro Ala Pro  
20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln Gln Gln Pro Pro Lys Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 484 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Met Asn Met Lys Lys Ala Thr Ile Ala Ala Thr Ala Gly Ile Ala Val
1          5          10
Thr Ala Phe Arg Ala Pro Thr Ile Arg Ser Ala Ser Thr Val Val Val
          20          25          30
Glu Ala Gly Asp Thr Leu Trp Gly Ile Ala Gln Ser Lys Gly Thr Thr
          35          40          45
Val Asp Ala Ile Lys Lys Ala Asn Asn Leu Thr Thr Asp Lys Ile Val
          50          55          60
Pro Gly Gln Lys Leu Gln Val Asn Asn Glu Val Ala Ala Ala Glu Lys
65          70          75          80
Thr Glu Lys Ser Val Ser Ala Thr Trp Leu Asn Val Arg Ser Gly Ala
          85          90          95
Gly Val Asp Asn Ser Ile Ile Thr Ser Ile Lys Gly Gly Thr Lys Val
          100          105          110
Thr Val Glu Thr Thr Glu Ser Asn Gly Trp His Lys Ile Thr Tyr Asn
          115          120          125
Asp Gly Lys Thr Gly Phe Val Asn Gly Lys Tyr Leu Thr Asp Lys Ala
          130          135          140
Val Ser Thr Pro Val Ala Pro Thr Gln Glu Val Lys Lys Glu Thr Thr
145          150          155          160
Thr Gln Gln Ala Ala Pro Ala Ala Glu Thr Lys Thr Glu Val Lys Gln
          165          170          175
Thr Thr Gln Ala Thr Thr Pro Ala Pro Lys Val Ala Glu Thr Lys Glu
          180          185          190
Thr Pro Val Val Asp Gln Asn Ala Thr Thr His Ala Val Lys Ser Gly
          195          200          205
Asp Thr Ile Trp Ala Leu Ser Val Lys Tyr Gly Val Ser Val Gln Asp
          210          215          220
Ile Met Ser Trp Asn Asn Leu Ser Ser Ser Ser Ile Tyr Val Gly Gln
225          230          235          240
Lys Leu Ala Ile Lys Gln Thr Ala Asn Thr Ala Thr Pro Lys Ala Glu
          245          250          255
Val Lys Thr Glu Ala Pro Ala Ala Glu Lys Gln Ala Ala Pro Val Val
          260          265          270
Lys Glu Asn Thr Asn Thr Asn Thr Ala Thr Thr Glu Lys Lys Glu Thr
          275          280          285
Ala Thr Gln Gln Gln Thr Ala Pro Lys Ala Pro Thr Glu Ala Ala Lys
          290          295          300

```

Pro Ala Pro Ala Pro Ser Thr Asn Thr Asn Ala Asn Lys Thr Asn Thr  
 305 310 315 320  
 Asn Thr Asn Thr Asn Thr Asn Thr Asn Asn Thr Asn Thr Asn Thr Pro  
 325 330 335  
 Ser Lys Asn Thr Asn Thr Asn Ser Asn Thr Asn Thr Asn Thr Asn Ser  
 340 345 350  
 Asn Thr Asn Ala Asn Gln Gly Ser Ser Asn Asn Asn Ser Asn Ser Ser  
 355 360 365  
 Ala Ser Ala Ile Ile Ala Glu Ala Gln Lys His Leu Gly Lys Ala Tyr  
 370 375 380  
 Ser Trp Gly Gly Asn Gly Pro Thr Thr Phe Asp Cys Ser Gly Tyr Thr  
 385 390 395 400  
 Lys Tyr Val Phe Ala Lys Ala Gly Ile Ser Leu Pro Arg Thr Ser Gly  
 405 410 415  
 Ala Gln Tyr Ala Ser Thr Thr Arg Ile Ser Glu Ser Gln Ala Lys Pro  
 420 425 430  
 Gly Asp Leu Val Phe Phe Asp Tyr Gly Ser Gly Ile Ser His Val Gly  
 435 440 445  
 Ile Tyr Val Gly Asn Gly Gln Met Ile Asn Ala Gln Asp Asn Gly Val  
 450 455 460  
 Lys Tyr Asp Asn Ile His Gly Ser Gly Trp Gly Lys Tyr Leu Val Gly  
 465 470 475 480  
 Phe Gly Arg Val

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala Val Ser Thr Pro Val Ala Pro Thr Gln Glu Val Lys Lys Glu Thr  
 1 5 10 15  
 Thr Thr Gln Ala  
 20

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Pro Thr Gln Glu Val Lys Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Val Lys Gln Thr Thr Gln Ala Thr Thr Pro Ala Pro Lys Val Ala Glu  
1 5 10 15  
Thr Lys Glu Thr Pro  
20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Thr Thr Pro Ala Pro Lys Val  
1 5

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Ala Ile Lys Gln Thr Ala Asn Thr Ala Thr Pro Lys Ala Glu Val  
1 5 10 15  
Lys Thr Glu Ala Pro  
20

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Thr Ala Thr Pro Lys Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Lys Lys Glu Thr Ala Thr Gln Gln Gln Thr Ala Pro Lys Ala Pro Thr  
1 5 10 15  
Glu Ala Ala Lys Pro  
20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln Gln Thr Ala Pro Lys Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 99 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr  
1 5 10 15



Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val  
                   20                                  25                                  30  
 Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu  
                   35                                  40                                  45  
 Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val  
                   50                                  55                                  60  
 Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln  
   65                                  70                                  75                                  80  
 Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr  
                   85                                  90                                  95  
 Pro Lys Thr

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr  
   1                  5                                  10

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gln Thr Gln Thr Pro Lys Thr  
   1                                  5

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Lys Ser Thr Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys  
1 5 10 15  
Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg  
20 25 30  
Glu Ala Val Ile Phe Lys Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln  
35 40 45  
Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr  
50 55 60  
Pro Lys Leu  
65

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Thr Gln Thr Pro Lys Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gln Gln Gln Gln Pro Ala Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gln Thr Ile Pro Ile Lys Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gln Ala Gln Thr Asn Ala Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Tyr Thr Thr Val Pro Lys Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Leu Thr Gly Thr Ser Lys Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:46:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu Gln Gln Thr Ala Gly Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:47:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gln Thr Gln Phe Ser Arg Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:48:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gln Thr Gln Gly Pro Tyr Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:49:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Pro Pro Gln Thr Pro Pro Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gln Ala Gln Pro Asn Lys Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gln Thr Gln Pro Ser Lys Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Ser Gln Thr Pro Leu Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Glu Thr Ser Val Pro Lys Cys  
1 5

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gln Thr Arg Asp Thr Lys Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Val Ser Thr Gln Lys Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Trp Thr Lys Asp Pro Lys Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Pro Asn Gln Lys Pro Lys Val  
1 5

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Gln Ser Leu Thr Thr Lys Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Gln Thr Gln Thr Asp Pro Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gln Leu Gln Asp Gly Lys Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln Glu Glu Gly Pro Lys Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asn Thr Asn Thr Ser Lys Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ala Thr Ala Ala Pro Lys Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gln Gly Glu Thr His Lys Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gln Gln Pro Ala Pro Ala Thr  
1 5



(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser Thr Gln Ser Ala Lys Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Gln Thr Thr Thr Pro Thr Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Gln Thr Gln Thr Pro Val Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Gln Pro Ala Ser Ser Lys Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Arg Pro Asp Thr Pro Arg Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Val Thr His Pro Pro Lys Val  
1 5

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ile Gln Pro Pro Lys Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ile Gln Pro Pro Lys Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln Thr Gln Val Ala Ala Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys Glu Ala Val Val Phe Val Thr Lys Leu Lys Arg Glu Val Cys Ala  
1 5 10 15  
Asp Pro Lys Lys Glu Trp Val Gln Thr Tyr Ile Lys Asn Leu Asp Arg  
20 25 30  
Gln Gln Gln Pro Pro Lys Ala  
35